



TABLE 5 (SEQ ID No:27 and SEQ ID No:28)

1 GGGGTGCANA GAAAGACAC CAGGCCCCAG CTGGAGGTG CTAACTCCAG AGGCCAGCAT CAGCAACTGG GCACAGAAAG

81 GAGCCGCTTG GGCAGGGACC <sup>1</sup>ATGGCAGGC CACATCCCTG GTGGCTGTGC GTTCTGGGGA CCTGTGGGG GCTCTCAGCT  
M A R P H P W L C V L G T L V G L S A

161 ACTCCAGCCC CCAAGAGCTG CCCAGAGAG CACTACTGGG CTCAGGANA GCTGTGCTGC CAGATGTGTG AGCCAGAAAC  
T P A P K S C P E R H Y W ~~W~~A Q G K L C C Q M C E P G T

241 ATTCCTCGTG AAGGACTGTG ACCAGCATAG AAAGGCTGCT CAGTGTGATC CTTCATACC GGGGCTCTCC TTCTCTCCTG  
F L V K D C D Q H R K A A Q C D P C I P G V S F S P D

321 ACCACCAAC CCGCCCCAC TGTAGAGCT GTGGCACTG TAACCTGTGT CTTCCTGTTG GCAACTGCAC CATCACTGCC  
H H T R P H C E S C R H C N S G L L V R N C T I T A

401 AATGCTGAGT GTGCTGTG CAACTGGCTGG CAGTGCAGGG ACAAGAGTG CACCGAGTGT GATCCTCTTC CAAACCTTC  
N A E C A C R N G W Q C R D K E C T E C D P L P N P S

481 GCTGACCGCT CGTGTCTCTC AGGCCCTGAG CCCACACCCT CAGCCCCACC ACTTAACCTTA TGTCAGTGAG ATGCTGAGG  
L T A R S S Q A L S P H P Q P T H L P Y V S E M L E A

561 CCAGGACAGC TGGGCACATG CAGACTCTGG CTGAQTTCAG GCAGCTGCCT GCCCGGACTC TCTCTACCA CTGGCCACCC  
R T A G H M Q T L A D F R Q L P A R T L S T H W P P

641 CAAGATCCC TGTGCAGCTC CGATTTTATT CGCATCCTTG TGAATCTCTC TGAATGTTT CTGTGTTTCA CCCTGGCCGG  
Q R S L C S S D F I R I L V I F S G M F L V F T L A G  
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721 GGGCCTGTTC CTCATCAAC GAAGAAATA TAGATCAAAC AAAGAGANA GTCTGTGGA GCCTGCAGAG CCTGTGCTT  
A L F L H Q R R K Y R S N K G E S P V E P A E P C R Y  
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801 ACAGCTGCCC CAGGGAGGAG GAGGGCAGCA CCATCCCCAT CCAGGAGGAT TACCGAANA CGGAGCCTGC CTGCTCCCC  
S C P R E E E G S T I P I Q E D Y R K P E P A C S P

881 <sup>\*</sup>TGAGCCAGCA CCTGCGGTAG CTGCATAACA GCCCTGGCCT CAACCCCCAC CCGCCGAC ATCCAAGGGA GAGTGAGACC

961 TGGCAGCCAC AACTGCACTC CCATCCTCTT GTCAAGGGCC TTTCCTGTGT ACACTGACA GAGTGCCCTTT TCGAGACTGG

1041 CAGGGACGAG GACAAATATG GATGAGGTGG AGAGTGGGA GCAGGAGCCC AGCCAAGCTGC CCGCGCCTGC AGGAGGGCGG

1121 GGGCTCTGCT TGTAAAGCAC ACTTCTCTGCT GCGAAGACC CACATGCTAC AAGACGGGCA AATTAAGTG ACAGATGACC